A1

SEQUENCE LISTING

<110>   NISHIMURA, SATORU

         KOIKE, AYUMI

<120>   CHOLINE MONOOXYGENASE GENE

<130>   0213-1431-0

<140>   09/534,995

<141>   2000-03-27

<150>   JP 273275/1999

<151>   1999-09-27

<160>   17

<170>   PatentIn version 3.1

<210>   1

<211>   1828

<212>   DNA

<213>   Chenopodium album

<220>

<221>   CDS

<222> (129)..(1427)

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acatcaat atg gca gca agt gca aca aca atg ttg ctg aaa tac cca aca   170
        Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr
          1   5   10

act gta tgt ggt ata cca aat tca tca tca aac aat gat act tca aat   218
Thr Val Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn
 15   20   25   30

aat ata gtc cca att cca caa act agt act aat aat ccg gta ctt aag   266
Asn Ile Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys
                 35   40   45

ttt cgt acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct ttt   314
Phe Arg Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe
                 50   55   60

cct tct tta aac acc acc act act ccg ccg tcg att caa tca ctt gtc   362
Pro Ser Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val
             65   70   75

cag gaa ttc gat ccg aag att ccg gct aag gat gct ctt acg cct cct   410
Gln Glu Phe Asp Pro Lys Ile Pro Ala Lys Asp Ala Leu Thr Pro Pro
         80   85   90

agc tct tgg tat act gac gct gct ttc tat gct cat gaa ctt gac cgt   458
Ser Ser Trp Tyr Thr Asp Ala Ala Phe Tyr Ala His Glu Leu Asp Arg
 95   100   105   110

atc ttt tat aag gga tgg caa gtc cca ggg tac agt gat caa att aag   506
Ile Phe Tyr Lys Gly Trp Gln Val Pro Gly Tyr Ser Asp Gln Ile Lys
                 115   120   125

gag cct aac caa tat ttc acc gga acg tta gga aat gtt gaa tat ttg   554
Glu Pro Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu
             130   135   140

gtg tgt cga gat ggt gaa gga aaa gtt cat gca ttt cac aac gtt tgc   602
Val Cys Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys
         145   150   155

acc cat cgt gct tcg att ctt gct tgt gga agt gga aaa aaa tcg tgt   650

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Thr His Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys
    160             165             170

ttt gtg tgc cct tac cat gga tgg gta ttt ggc atg aat gga tcg ctt     698
Phe Val Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu
175             180             185             190

aca aaa gct tcc aaa gca acc gaa gaa cag tca ctt gat ccc gat gaa     746
Thr Lys Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu
            195             200             205

ctt ggg ctt gta ccc ctg aaa gtt gca gta tgg ggc cca ttt ata ctc     794
Leu Gly Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu
            210             215             220

ata agt ttg gac aga tca agc ctt gaa gta ggt gat gtt gga tct gaa     842
Ile Ser Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu
            225             230             235

tgg ctt ggt agt tgt gct gaa gat gtt aag gcc cat gct ttt gac cct     890
Trp Leu Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro
    240             245             250

aat tta cag ttc atc aat agg agt gaa ttt cca atg gaa tct aat tgg     938
Asn Leu Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp
255             260             265             270

aag att ttc agt gac aac tat ttg gat agc tcg tac cat gtt cct tat     986
Lys Ile Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr
            275             280             285

gca cac aag tac tat gct act gaa ctc gac ttt gat act tac caa act    1034
Ala His Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr
            290             295             300

gat atg atc gga aac gtc acg att caa aga gtg gca ggg agt tca aac    1082
Asp Met Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn
            305             310             315

aat ggt ttt aat aga ctt gga tct caa gca ttc tat gct ttt gca tac    1130
Asn Gly Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr
    320             325             330

cct aac ttt gct gtg gaa agg tat ggc cct tgg atg aca aca atg cac    1178
Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His
335             340             345             350

att ctt cca tta gga cca agg aaa tgc aaa tta gtg gtg gac tac tac    1226
Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr
            355             360             365

att gaa aaa tca aag ctg gac gac aag gat tac atc gag aag ggc att    1274
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Ile Glu Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile
            370                 375                 380

gca atc aat gat aat gta cag aaa gaa gat gtg gtg ttg tgt gaa agt        1322
Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser
            385                 390                 395

gtc caa aaa ggg ttg gaa aca cca gca tat cgt agt gga aga tat gtg        1370
Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val
    400                 405                 410

atg cca att gag aaa gga atc cat cat ttc cac tgc tgg ttg cac caa        1418
Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln
415                 420                 425                 430

gta ttg aag tgattgcagc agatcatcag atgttcgttt cttcttgtat            1467
Val Leu Lys


tggaattgga tattatgatt aataagtaaa attataatgt cataatgtag ttgagattgt      1527

tgctagagtt gagcgtatgc tcctcatgca ctacttagtt atcaagtgtg tatgtctttg      1587

gtcatgggca aaatgtatgt ttcttgctag aatttatata ttatggtgct aatgtccaat      1647

ataaataaaa accatagcac ccctttaatt ccctacttag gtttatatcc catttatttt      1707

cgggggatct atgagataga ttgtctatga acattatttt tcgactcgtg tatggtattc      1767

atcccttgtg tagggtgaag taaacattga gtgtatgaag ttttcattga gtttctgctt      1827

t                                                                      1828
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<210> 2

<211> 433

<212> PRT

<213> Chenopodium album

<400> 2

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Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
1               5                   10                  15


Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
                20                  25                  30
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Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg
        35              40                  45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
        50              55                  60

Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65                  70                  75                      80

Phe Asp Pro Lys Ile Pro Ala Lys Asp Ala Leu Thr Pro Pro Ser Ser
                85                  90                  95

Trp Tyr Thr Asp Ala Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
            100                 105                 110

Tyr Lys Gly Trp Gln Val Pro Gly Tyr Ser Asp Gln Ile Lys Glu Pro
            115                 120                 125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
        130             135                 140

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145                 150                 155                 160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
                165                 170                 175

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
            180                 185                 190

Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
        195                 200                 205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
        210                 215                 220

Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu
225                 230                 235                 240
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```
Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
            245             250             255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
            260             265             270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
            275             280             285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
    290             295             300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Asn Gly
305             310             315             320

Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr Pro Asn
            325             330             335

Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His Ile Leu
            340             345             350

Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr Ile Glu
            355             360             365

Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile Ala Ile
    370             375             380

Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser Val Gln
385             390             395             400

Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val Met Pro
            405             410             415

Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln Val Leu
            420             425             430

Lys
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<210> 3

<211> 1651

<212> DNA

<213> Chenopodium album

<220>

<221> CDS

<222> (119)..(1423)

<223>

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aaattataac aacaaaggga agtgtttagt tattgcttga tcatcatata atatcaac   118

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atg tca gca agt gca aca aca atg ttg ctg aaa tac cca aca act gta          166
Met Ser Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
1               5                   10                  15

tgt ggt ata cca aat tca tca tca aac aat gat act tca aat aac atc          214
Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
                20                  25                  30

gtc cca att cca caa act agt act aat aat ccg gta ctt aag ttt cgt          262
Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg
            35                  40                  45

acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct ttt cct tct          310
Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
        50                  55                  60

tta agt acc acc act act ccg ccg tcg att caa tca ctt gtc cag gaa          358
Leu Ser Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65                  70                  75                  80

ttc gat ccg agg att ctg gcc gag gat gct ctc acg cct cct agc tct          406
Phe Asp Pro Arg Ile Leu Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser
                85                  90                  95

tgg tat act gaa cct gcc ttc tat gct cat gaa ctt gac cgt atc ttt          454
Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
                100                 105                 110
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tac aaa gga tgg caa gtc gca ggg tac agc gat caa att aag gag cct     502
Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro
        115             120             125

aac caa tat ttc acc gga acg tta gga aat gtt gaa tat ttg gtg tgt     550
Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
        130             135             140

cga gat ggt gaa gga aaa gtt cat gca ttt cac aat gtt tgc act cat     598
Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145             150             155             160

cgt gct tcg att ctt gct tgt gga agt ggc aaa aaa tcg tgt ttc gta     646
Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
                165             170             175

tgc cct tac cat ggt tgg gta ttt ggc atg aat gga tca ctt acg aaa     694
Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
        180             185             190

gct tcc aaa gca acc gaa gaa cag tcc ctt gat ccc gat gaa ctt ggg     742
Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
        195             200             205

ctt gta ccc ctg aaa gtt gca gta tgg ggc cca ttt ata ctc atc agt     790
Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
        210             215             220

ttg gac aga tca agc ctt gaa gta ggc gat gtt gga tct gaa tgg ctt     838
Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu
225             230             235             240

ggt agt tgt gct gaa gat gtt aag gcc cat gct ttt gac cct aat ttg     886
Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
                245             250             255

cag ttc atc aat agg agt gaa ttt cca atg gaa tct aat tgg aag att     934
Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
                260             265             270

ttc agt gac aac tac ttg gat agc tcg tac cat gtt cct tat gca cac     982
Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
                275             280             285

aag tac tat gca act gaa ctc gac ttt gat act tat caa acc gat atg    1030
Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
        290             295             300

att gga aat gtc acg att caa aga gtg gcg ggg agt tca aac aag cca    1078
Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Lys Pro
305             310             315             320
```

```
gat ggt ttt gat aga ctt gga tct caa gca ttc tat gct ttt gca tac    1126
Asp Gly Phe Asp Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr
            325             330             335

cct aac ttt gct gtg gaa agg tat ggc cct tgg atg aca aca atg cat    1174
Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His
            340             345             350

att ctt cca tta gga cca aga aaa tgc aaa tta gtg gtg gac tac tat    1222
Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr
            355             360             365

att gaa aaa tca atg ctg gac gac aag gat tac atc gag aag ggc ata    1270
Ile Glu Lys Ser Met Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile
    370             375             380

gca atc aat gat aat gta cag aaa gaa gat gtg gtg ttg tgt gaa agt    1318
Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser
385             390             395             400

gtc caa aaa ggg ttg gag aca cca gca tat cgt agt gga aga tat gtg    1366
Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val
            405             410             415

atg cca att gag aaa gga atc cat cat ttc cac tgt tgg ttg cac caa    1414
Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln
            420             425             430

gta ttg aag tgatagcagc agatcagatg ttcgtttctt aatttccttt          1463
Val Leu Lys
            435

tattggaact ggataattat aataataata agtaaaaaag taaaattata atgtcatgta  1523

gttgagattg ttgctagagt tgagcgtatg ctcctcatgc acttagttat caagtgtgta  1583

tgtgtttggt catggacaaa atgtttcttg ctagaattta tcatattata aggtgctaat  1643

gtccaata                                                          1651


<210>  4

<211>  435

<212>  PRT

<213>  Chenopodium album


<400>  4
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Met Ser Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
1               5                   10                  15

Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
            20                  25                  30

Val Pro Ile Pro Gln Thr Ser Thr Asn Asn Pro Val Leu Lys Phe Arg
            35              40                  45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
    50                  55                  60

Leu Ser Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65                  70                  75                  80

Phe Asp Pro Arg Ile Leu Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser
            85                  90                  95

Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
            100             105             110

Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro
            115             120             125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
    130             135             140

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145             150             155             160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
            165             170             175

Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
            180             185             190

Ala Ser Lys Ala Thr Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
    195             200             205
```

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Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
210   215   220

Leu Asp Arg Ser Ser Leu Glu Val Gly Asp Val Gly Ser Glu Trp Leu
225   230   235   240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
245   250   255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
260   265   270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
275   280   285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
290   295   300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Lys Pro
305   310   315   320

Asp Gly Phe Asp Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr
325   330   335

Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His
340   345   350

Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr
355   360   365

Ile Glu Lys Ser Met Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile
370   375   380

Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser
385   390   395   400

Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val
405   410   415

```
Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln
            420                 425                 430


Val Leu Lys
        435


<210>  5

<211>  1712

<212>  DNA

<213>  Chenopodium album


<220>

<221>  CDS

<222>  (133)..(1431)

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tataacatca at atg gca gca agt gca aca aca atg ttg ctg aaa tac cca     171
              Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro
              1               5                   10

aca act gta tgt ggt ata cca aat tca tca tca aac aat gat act tca       219
Thr Thr Val Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser
    15                  20                  25

aat aac atc gtc cca att cca caa act att act aat aat ccg gta ctt       267
Asn Asn Ile Val Pro Ile Pro Gln Thr Ile Thr Asn Asn Pro Val Leu
30                  35                  40                  45

aag ttt cgt acc cct aat aaa acc att aac gcc gtc gct gcc ccg gct       315
Lys Phe Arg Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala
                50                  55                  60

ttt cct tct tta aac acc acc act act ccg ccg tca att caa tca ctt       363
Phe Pro Ser Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu
            65                  70                  75
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gtc cag gaa ttc gat ccg agg att ccg gcc gag gat gct ctt acg cct       411
Val Gln Glu Phe Asp Pro Arg Ile Pro Ala Glu Asp Ala Leu Thr Pro
        80                  85                  90

cct agc tct tgg tat act gaa cct gct ttc tat gct cat gaa ctt gac       459
Pro Ser Ser Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp
        95                 100                 105

cgt atc ttt tac aag gga tgg caa gtc gca ggg tac agt gat caa att       507
Arg Ile Phe Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile
110                 115                 120                 125

aag gag cct aac caa tat ttc acc gga acg tta gga aat gtt gaa tat       555
Lys Glu Pro Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr
                    130                 135                 140

ttg gtg tgt cga gat ggt gaa ggt aaa gtt cat gca ttt cac aac gtt       603
Leu Val Cys Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val
                145                 150                 155

tgc acc cat cgt gct tcg att ctt gct tgt gga agc gga aaa aaa tcg       651
Cys Thr His Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser
            160                 165                 170

tgt ttt gta tgc cct tac cat gga tgg gta ttt ggc atg aat gga tcg       699
Cys Phe Val Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser
        175                 180                 185

ctt aca aaa gct tcc aaa gca agc gaa gaa cag tca ctt gat ccc gat       747
Leu Thr Lys Ala Ser Lys Ala Ser Glu Glu Gln Ser Leu Asp Pro Asp
190                 195                 200                 205

gaa ctt ggg ctt gta ccc ctg aaa gtt gca gta tgg ggc cca ttt ata       795
Glu Leu Gly Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile
                    210                 215                 220

ctc atc agt ttg gac aga tca agc ctt gaa gta gat gat gtt gga tct       843
Leu Ile Ser Leu Asp Arg Ser Ser Leu Glu Val Asp Asp Val Gly Ser
                225                 230                 235

gaa tgg ctt ggt agt tgt gct gaa gat gtt aag gcc cat gct ttt gac       891
Glu Trp Leu Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp
            240                 245                 250

cct aat ttg cag ttc atc aat agg agt gaa ttt cca atg gaa tct aat       939
Pro Asn Leu Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn
        255                 260                 265

tgg aag att ttc agt gac aac tat ttg gat agc tcg tac cat gtt cct       987
Trp Lys Ile Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro
270                 275                 280                 285
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tat gca cac aag tac tat gct act gaa ctc gac ttt gat act tac caa        1035
Tyr Ala His Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln
            290             295             300

act gat atg atc gga aat gtc acg att caa aga gtg gca ggg agt tca        1083
Thr Asp Met Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser
            305             310             315

aac aat ggt ttt aat aga ctt gga tct caa gca ttc tac gct ttt gca       1131
Asn Asn Gly Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala
            320             325             330

tac cct aac ttt gct gtg gaa agg tat ggc cct tgg atg aca aca atg       1179
Tyr Pro Asn Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met
            335             340             345

cac att ctt cca tta gga cca agg aaa tgc aaa tta gtg gtg gac tac       1227
His Ile Leu Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr
350             355             360             365

tat att gaa aaa tca aag ctg gac gac aag gat tac atc gag aag ggc       1275
Tyr Ile Glu Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly
            370             375             380

ata gca atc aat gat aat gta cag aaa gaa gat gtg gtg ttg tgt gaa       1323
Ile Ala Ile Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu
            385             390             395

agt gtc caa aaa ggg ttg gag aca cct gcg tat cgt agt gga aga tat       1371
Ser Val Gln Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr
            400             405             410

gtg atg cca att gag aaa gga atc cat cat ttc cac tgt tgg ttg cac       1419
Val Met Pro Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His
            415             420             425

caa gta ttg aag tgattgcagc agatcagatg ttcgtttctt aatttccttt          1471
Gln Val Leu Lys
430

tattggaatt ggatgattgt tataataata agtaaaatta taatgtcatg tagttgagat    1531

tgttgctaga gttgagcgta tgctcctcat gcacttagtt atcaagtgtg tatgtgtttg    1591

gtcatgggca aaatgtattt tcttgctaga atttgttata ttatggtgct aatgtccaat    1651

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g                                                                     1712


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Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
            20   25   30

Val Pro Ile Pro Gln Thr Ile Thr Asn Asn Pro Val Leu Lys Phe Arg
        35   40   45

Thr Pro Asn Lys Thr Ile Asn Ala Val Ala Ala Pro Ala Phe Pro Ser
    50   55   60

Leu Asn Thr Thr Thr Thr Pro Pro Ser Ile Gln Ser Leu Val Gln Glu
65   70   75   80

Phe Asp Pro Arg Ile Pro Ala Glu Asp Ala Leu Thr Pro Pro Ser Ser
            85   90   95

Trp Tyr Thr Glu Pro Ala Phe Tyr Ala His Glu Leu Asp Arg Ile Phe
            100   105   110

Tyr Lys Gly Trp Gln Val Ala Gly Tyr Ser Asp Gln Ile Lys Glu Pro
        115   120   125

Asn Gln Tyr Phe Thr Gly Thr Leu Gly Asn Val Glu Tyr Leu Val Cys
    130   135   140

Arg Asp Gly Glu Gly Lys Val His Ala Phe His Asn Val Cys Thr His
145   150   155   160

Arg Ala Ser Ile Leu Ala Cys Gly Ser Gly Lys Lys Ser Cys Phe Val
            165   170   175

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Cys Pro Tyr His Gly Trp Val Phe Gly Met Asn Gly Ser Leu Thr Lys
        180             185                 190

Ala Ser Lys Ala Ser Glu Glu Gln Ser Leu Asp Pro Asp Glu Leu Gly
        195             200                 205

Leu Val Pro Leu Lys Val Ala Val Trp Gly Pro Phe Ile Leu Ile Ser
210             215                 220

Leu Asp Arg Ser Ser Leu Glu Val Asp Asp Val Gly Ser Glu Trp Leu
225                 230                 235                 240

Gly Ser Cys Ala Glu Asp Val Lys Ala His Ala Phe Asp Pro Asn Leu
                245                 250                 255

Gln Phe Ile Asn Arg Ser Glu Phe Pro Met Glu Ser Asn Trp Lys Ile
                260                 265                 270

Phe Ser Asp Asn Tyr Leu Asp Ser Ser Tyr His Val Pro Tyr Ala His
        275                 280                 285

Lys Tyr Tyr Ala Thr Glu Leu Asp Phe Asp Thr Tyr Gln Thr Asp Met
290                 295                 300

Ile Gly Asn Val Thr Ile Gln Arg Val Ala Gly Ser Ser Asn Asn Gly
305                 310                 315                 320

Phe Asn Arg Leu Gly Ser Gln Ala Phe Tyr Ala Phe Ala Tyr Pro Asn
                325                 330                 335

Phe Ala Val Glu Arg Tyr Gly Pro Trp Met Thr Thr Met His Ile Leu
                340                 345                 350

Pro Leu Gly Pro Arg Lys Cys Lys Leu Val Val Asp Tyr Tyr Ile Glu
        355                 360                 365

Lys Ser Lys Leu Asp Asp Lys Asp Tyr Ile Glu Lys Gly Ile Ala Ile
        370                 375                 380
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Asn Asp Asn Val Gln Lys Glu Asp Val Val Leu Cys Glu Ser Val Gln
385   390   395   400

Lys Gly Leu Glu Thr Pro Ala Tyr Arg Ser Gly Arg Tyr Val Met Pro
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Ile Glu Lys Gly Ile His His Phe His Cys Trp Leu His Gln Val Leu
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Lys

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Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
1               5                   10                  15

tgt ggt ata cca aat tca tca tca aac aat gat act tca aat aac atc        96
Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
                20                  25                  30

gtc cca att cca caa act att act aat aat c                            127
Val Pro Ile Pro Gln Thr Ile Thr Asn Asn
            35                  40
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Met Ala Ala Ser Ala Thr Thr Met Leu Leu Lys Tyr Pro Thr Thr Val
1               5                   10                  15


Cys Gly Ile Pro Asn Ser Ser Ser Asn Asn Asp Thr Ser Asn Asn Ile
                20                  25                  30


Val Pro Ile Pro Gln Thr Ile Thr Asn Asn
            35                  40
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